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#12

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Application Serial Number: 10/019,980A
Source: PCT10
Date Processed by STIC: 10/24/02

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PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

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Revised 01/29/2002



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PCT 09
10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/019,980A

DATE: 10/24/2002

TIME: 16:07:59

Input Set : A:\EP.txt

Output Set: N:\CRF4\10242002\J019980A.raw

3 <110> APPLICANT: Berthelsen, Jens
4 Toma, Salvatore
5 Isacchi, Antonella
7 <120> TITLE OF INVENTION: Tankyrase Homolog Protein (THP), Nucleic Acids, And Methods
8 Related To The Same
10 <130> FILE REFERENCE: PHRM0373
12 <140> CURRENT APPLICATION NUMBER: 10/019,980A
C--> 13 <141> CURRENT FILING DATE: 1999-07-03
15 <150> PRIOR APPLICATION NUMBER: 09/350,982
16 <151> PRIOR FILING DATE: 1999-07-09
18 <150> PRIOR APPLICATION NUMBER: PCT/EP00/06609
19 <151> PRIOR FILING DATE: 2000-07-03
21 <160> NUMBER OF SEQ ID NOS: 10
23 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

25 <210> SEQ ID NO: 1
26 <211> LENGTH: 20
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial Sequence
30 <220> FEATURE:
31 <223> OTHER INFORMATION: PCR Primers
33 <400> SEQUENCE: 1
E--> 34 gagtatttgt tacaacacgg
35 20
38 <210> SEQ ID NO: 2
39 <211> LENGTH: 18
40 <212> TYPE: DNA
41 <213> ORGANISM: Artificial Sequence
43 <220> FEATURE:
44 <223> OTHER INFORMATION: PCR Primers
46 <400> SEQUENCE: 2
E--> 47 aatctccttc agctcctt
48 18
51 <210> SEQ ID NO: 3
52 <211> LENGTH: 4512
53 <212> TYPE: DNA
54 <213> ORGANISM: Homo sapiens
56 <220> FEATURE:
57 <221> NAME/KEY: misc_feature
58 <222> LOCATION: (1124)..(1124)

*Wrapped nucleics throughout.
See error summary sheet item 1.*

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59 <223> OTHER INFORMATION: N is any nucleic acid

62 <220> FEATURE:

63 <221> NAME/KEY: misc_feature

64 <222> LOCATION: (2672)..(2672)

65 <223> OTHER INFORMATION: N is any nucleic acid

68 <400> SEQUENCE: 3

E--> 69 gaattccgcg gcggccagga tcatgtcggg tcgccgctgc gccggcgggg gagcggcctg
70 60

E--> 72 cgcgagcgcc gcggccgagg ccgtggagcc ggccgccga gagctgttcg aggcgtgccg
73 120

E--> 75 caacggggac gtggaacgag tcaagaggct ggtgacgcct gagaaggtga acagccgcga
76 180

E--> 78 cacggcgggc aggaaatcca ccccgctgca cctcgccgca ggttttgggc ggaaagacgt
79 240

E--> 81 agttgaatat ttgcttcaga atggtgcaaa tgtccaagca cgtgatgatg ggggccttat
82 300

E--> 84 tcctcttcat aatgcatgct cttttggtca tgctgaagta gtcaatctcc ttttgcgaca
85 360

E--> 87 tgggtgcagac cccaatgctc gagataattg gaattatact cctctccatg aagctgcaat
88 420

E--> 90 taaaggaaag attgatgttt gcattgtgct gttacagcat ggagctgagc caaccatccg
91 480

E--> 93 aaatacagat ggaaggacag cattggattt agcagatcca tctgccaaag cagtgttac
94 540

E--> 96 tgggtgaatat aagaaagatg aactcttaga aagtgccagg agtggcaatg aagaaaaaat
97 600

E--> 99 gatggctcta ctcacaccat taaatgtcaa ctgccacgca agtgatggca gaaagtcaac
100 660

E--> 102 tccattacat ttggcagcag gatataacag agtaaagatt gtacagctgt tactgcaaca
103 720

E--> 105 tggagctgat gtccatgcta aagataaagg tgatctggta ccattacaca atgcctgttc
106 780

E--> 108 ttatgggtcat tatgaagtaa ctgaactttt ggtcaagcat ggtgcctgtg taaatgcaat
109 840

E--> 111 ggacttgttg caattcactc ctcttcatga ggcagcttct aagaacaggg ttgaagtatg
112 900

E--> 114 ttctcttctc ttaagttatg gtgcagaccc aacactgctc aattgtcaca ataaaagtgc
115 960

E--> 117 tatagacttg gctcccacac cacagttaaa agaaagatta gcatatgaat ttaaaggcca
118 1020

E--> 120 ctcgttgctg caagctgcac gagaagctga tgttactcga atcaaaaaac atctctctct
121 1080

E--> 123 ggaaatggtg aatttcaagc atcctcaaac acatgaaaca gcantgcatt gtgctgctgc
124 1140

E--> 126 atctccatat cccaaaagaa agcaaatatg tgaactgttg ctaagaaaag gagcaamcat
127 1200

E--> 129 caatgaaaag actaaagaat tcttgactcc tctgcacgtg gcattctgaga aagctcataa
130 1260

E--> 132 tgatrttgtt gaagtagtgg tgaaacatga agcaaagggt aatgctctgg ataactctgg

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133 1320
E--> 135 tcagacttct ctacacagag ctgcatattg tggtcattcta caaacctgcc gcctactcct
136 1380
E--> 138 gagctatggg tgtgatccta acattatatc ccttcagggc tttactgctt tacagatggg
139 1440
E--> 141 aaatgaaaat gtacagcaac tcctccaaga gggatatctca ttaggtaatt cagaggcaga
142 1500
E--> 144 cagacaattg ctggaagctg caaaggctgg agatgtcgaa actgtaaaaa aactgtgtac
145 1560
E--> 147 tgttcagagt gtcaactgca gagacattga agggcgctcag tctacaccac ttcattttgc
148 1620
E--> 150 agctgggtat aacagagtgt ccgtgggtgga atatctgcta cagcatggag ctgatgtgca
151 1680
E--> 153 tgctaaagat aaagrrgsc tttgtacctt gcacaatgca tgttcttatg gacattatga
154 1740
E--> 156 agttgcagaa cttcttggtta aacatggagc agtagttaat gtagctgatt tatggaaatt
157 1800
E--> 159 tacaccttta catgaagcag cagcaaaaagg aaaatatgaa atttgcaaac ttctgctcca
160 1860
E--> 162 gcatgggtgca gaccctacaa aaaaaaacag ggatggaaat actcctttgg atcttggtta
163 1920
E--> 165 agatggagat acagatatc aagatctgct taggggagat gcagctttgc tagatgctgc
166 1980
E--> 168 caagaagagt tgtttagcca gagtgaagaa gttgtcttct cctgataatg taaattgccg
169 2040
E--> 171 cgatacccaa ggcagacatt caacaccttt acatttagca gctgggttata ataatttaga
172 2100
E--> 174 agttgcagag tatttggttac aacacggagc tgatgtgaat gcccaagaca aaggaggact
175 2160
E--> 177 tattccttta cataatgcag catcttacgg gcatgtagat gtagcagctc tactaataaa
178 2220
E--> 180 gtataatgca tgtgtcaatg ccacggacaa atgggctttc acacctttgc acgaagcagc
181 2280
E--> 183 ccaaaaggga cgaacacagc tttgtgcttt gktgctagcc catggagctg acccgactct
184 2340
E--> 186 taaaaatcag gaaggacaaa cacctttaga tttagtttca gcggatgatg tcagcgctct
187 2400
E--> 189 tctgacagca gccatgcccc catctgctct gccctcttgt tacaagctc aagtgtcaa
190 2460
E--> 192 tgggtgtgaga agcccaggag ccaactgcaga tgctctctct tcagggtccat ctagcccatc
193 2520
E--> 195 aagcctttct gcagccagca gtcttgacaa cttatctggg agtttttcag aactgtcttc
196 2580
E--> 198 agtagttagt tcaagtggaa cagaggggtgc ttccagtttg gagaaaaagg aggttccagg
199 2640
E--> 201 agtagatttt agcataactc aattcgtaag gnatcttgga cttgagcacc taatggatat
202 2700
E--> 204 atttgagaga gaacagatca ctttggtatg attagttgag atggggcaca aggagctgaa
205 2760

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E--> 207 ggagattgga atcaatgctt atggacatag gcacaaacta attaaaggag tcgagagact
208 2820

E--> 210 tatctccgga caacaaggct ttaaccata tttaactttg aacacctctg gtagtggaac
211 2880

E--> 213 aattcttata gatctgtctc ctgatgataa agagtttcag tctgtggagg aagagatgca
214 2940

E--> 216 aagtacagtt cgagagcaca gagatggagg tcatgcaggt ggaatcttca acagatacaa
217 3000

E--> 219 tattctcaag attcagaagg tttgtaacaa gaaactatgg gaaagataca ctcaccggag
220 3060

E--> 222 aaaagaagtt tctgaagaaa accacaacca tgccaatgaa cgaatgctat ttcatgggctc
223 3120

E--> 225 tccttttctg aatgcaatta tccacaaagg ctttgatgaa aggcattgct acataggtgg
226 3180

E--> 228 tatgtttgga gctggcattt attttgctga aaactcttcc aaaagcaatc aatatgtata
229 3240

E--> 231 tggaattgga ggaggtactg ggtgtccagt tcacaaagac agatcttggt acatttgcca
232 3300

E--> 234 caggcagctg ctcttttgcc gggtaacctt gggaaagtct ttcttgagct tcagtgcaat
235 3360

E--> 237 gaaaatggca cattctctc cagggtcatca ctcagtcact ggtaggcccc gtgtaaattg
238 3420

E--> 240 cctagcatta gctgaatatg ttatttacag aggagaacag gcttatcctg agtatttaat
241 3480

E--> 243 tacttaccag attatgaggc ctgaagggtat ggtcgatgga taaatagtta ttttaagaaa
244 3540

E--> 246 ctaattccac tgaacctaaa atcatcaaag cagcagtggc ctctacgttt tactcctttg
247 3600

E--> 249 ctgaaaaaaa atcatcttgc ccacaggect gtggcaaaag gataaaaatg tgaacgaagt
250 3660

E--> 252 ttaacattct gacttgataa agctttaata atgtacagt ttttctaaat atttcctggt
253 3720

E--> 255 ttttcagcac ttttaacagat gccattccag gttaaactgg gttgtctgta ctaaattata
256 3780

E--> 258 aacagagtta acttgaacct tttatatggt atgcattgat tctaacaaac tgtaatgccc
259 3840

E--> 261 tcaacagAAC taattttact aatacaatac tgtgttcttt aaaacacagc atttacactg
262 3900

E--> 264 aatacaattt catttgtaaa actgtaaata agagcttttg tactagcccc gtattttatt
265 3960

E--> 267 acattgcttt gtaatatata tctgttttag aactgcagcg gtttacaaaa tttttcata
268 4020

E--> 270 tgtattgttc atctatactt gcatcttaca tcgtcatgat tgagtgatct ttacatttga
271 4080

E--> 273 ttccagaggc tatgttcagt tgtagttgg gaaagattga gttatcagat ttaatttgcc
274 4140

E--> 276 gatgggagcc tttatctgtc attagaaatc tttctcattt aagaacttat gaatatgctg
277 4200

E--> 279 aagatttaat ttgtgatacc tttgtatgta tgagacacat tccaaagAAC tctaactatg

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280 4260
E--> 282 ataggtcctg attactaaag aagcttcttt actggcctca atttctagct ttcattgttg
283 4320
E--> 285 aaaattttct gcagtccttc tgtgaaaatt agagcaaagt gctcctgttt tttagagaaa
286 4380
E--> 288 ctaaattcttg ctgttgaaca attattgtgt tcttttcatg gaacataagt aggatgttac
289 4440
E--> 291 atttccaggg tgggaagggg aatcctaaat catttcccaa tctattctaa ttaccttaaa
292 4500
E--> 294 tctaaagggg aa
295 4512
298 <210> SEQ ID NO: 4
299 <211> LENGTH: 3498
300 <212> TYPE: DNA
301 <213> ORGANISM: Artificial Sequence
303 <220> FEATURE:
304 <223> OTHER INFORMATION: PCR Primers
306 <220> FEATURE:
307 <221> NAME/KEY: CDS
308 <222> LOCATION: (1)..(3498)
309 <223> OTHER INFORMATION:
312 <220> FEATURE:
313 <221> NAME/KEY: misc_feature
314 <222> LOCATION: (1102)..(1102)
315 <223> OTHER INFORMATION: N is any nucleic acid
W--> 318 <220>
319 <221> NAME/KEY: misc_feature
320 <222> LOCATION: (2650)..(2650)
321 <223> OTHER INFORMATION: N is any nucleic acid
324 <400> SEQUENCE: 4
E--> 325 atg tcg ggt cgc cgc tgc gcc ggc ggg gga gcg gcc tgc gcg agc gcc
326 48
327 Met Ser Gly Arg Arg Cys Ala Gly Gly Gly Ala Ala Cys Ala Ser Ala
328 1 5 10 15
E--> 330 gcg gcc gag gcc gtg gag ccg gcc gcc cga gag ctg ttc gag gcg tgc
331 96
332 Ala Ala Glu Ala Val Glu Pro Ala Ala Arg Glu Leu Phe Glu Ala Cys
333 20 25 30
E--> 335 cgc aac ggg gac gtg gaa cga gtc aag agg ctg gtg acg cct gag aag
336 144
337 Arg Asn Gly Asp Val Glu Arg Val Lys Arg Leu Val Thr Pro Glu Lys
338 35 40 45
E--> 340 gtg aac agc cgc gac acg gcg ggc agg aaa tcc acc ccg ctg cac ctc
341 192
342 Val Asn Ser Arg Asp Thr Ala Gly Arg Lys Ser Thr Pro Leu His Leu
343 50 55 60
E--> 345 gcc gca ggt ttt ggg cgg aaa gac gta gtt gaa tat ttg ctt cag aat
346 240
347 Ala Ala Gly Phe Gly Arg Lys Asp Val Val Glu Tyr Leu Leu Gln Asn

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      348 65              70              75              80
E--> 350 ggt gca aat gtc caa gca cgt gat gat ggg ggc ctt att cct ctt cat
      351 288
      352 Gly Ala Asn Val Gln Ala Arg Asp Asp Gly Gly Leu Ile Pro Leu His
      353              85              90              95
E--> 355 aat gca tgc tct ttt ggt cat gct gaa gta gtc aat ctc ctt ttg cga
      356 336
      357 Asn Ala Cys Ser Phe Gly His Ala Glu Val Val Asn Leu Leu Leu Arg
      358              100              105              110
E--> 360 cat ggt gca gac ccc aat gct cga gat aat tgg aat tat act cct ctc
      361 384
      362 His Gly Ala Asp Pro Asn Ala Arg Asp Asn Trp Asn Tyr Thr Pro Leu
      363              115              120              125
E--> 365 cat gaa gct gca att aaa gga aag att gat gtt tgc att gtg ctg tta
      366 432
      367 His Glu Ala Ala Ile Lys Gly Lys Ile Asp Val Cys Ile Val Leu Leu
      368              130              135              140
E--> 370 cag cat gga gct gag cca acc atc cga aat aca gat gga agg aca gca
      371 480
      372 Gln His Gly Ala Glu Pro Thr Ile Arg Asn Thr Asp Gly Arg Thr Ala
      373 145              150              155              160
E--> 375 ttg gat tta gca gat cca tct gcc aaa gca gtg ctt act ggt gaa tat
      376 528
      377 Leu Asp Leu Ala Asp Pro Ser Ala Lys Ala Val Leu Thr Gly Glu Tyr
      378              165              170              175
E--> 380 aag aaa gat gaa ctc tta gaa agt gcc agg agt ggc aat gaa gaa aaa
      381 576
      382 Lys Lys Asp Glu Leu Leu Glu Ser Ala Arg Ser Gly Asn Glu Glu Lys
      383              180              185              190
E--> 385 atg atg gct cta ctc aca cca tta aat gtc aac tgc cac gca agt gat
      386 624
      387 Met Met Ala Leu Leu Thr Pro Leu Asn Val Asn Cys His Ala Ser Asp
      388              195              200              205
E--> 390 ggc aga aag tca act cca tta cat ttg gca gca gga tat aac aga gta
      391 672
      392 Gly Arg Lys Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn Arg Val
      393              210              215              220
E--> 395 aag att gta cag ctg tta ctg caa cat gga gct gat gtc cat gct aaa
      396 720
      397 Lys Ile Val Gln Leu Leu Leu Gln His Gly Ala Asp Val His Ala Lys
      398 225              230              235              240
E--> 400 gat aaa ggt gat ctg gta cca tta cac aat gcc tgt tct tat ggt cat
      401 768
      402 Asp Lys Gly Asp Leu Val Pro Leu His Asn Ala Cys Ser Tyr Gly His
      403              245              250              255
E--> 405 tat gaa gta act gaa ctt ttg gtc aag cat ggt gcc tgt gta aat gca
      406 816
      407 Tyr Glu Val Thr Glu Leu Leu Val Lys His Gly Ala Cys Val Asn Ala
      408              260              265              270

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E--> 410 atg gac ttg tgg caa ttc act cct ctt cat gag gca gct tct aag aac
      411 864
      412 Met Asp Leu Trp Gln Phe Thr Pro Leu His Glu Ala Ala Ser Lys Asn
      413          275          280          285
E--> 415 agg gtt gaa gta tgt tct ctt ctc tta agt tat ggt gca gac cca aca
      416 912
      417 Arg Val Glu Val Cys Ser Leu Leu Leu Ser Tyr Gly Ala Asp Pro Thr
      418      290          295          300
E--> 420 ctg ctc aat tgt cac aat aaa agt gct ata gag ttg gct ccc aca cca
      421 960
      422 Leu Leu Asn Cys His Asn Lys Ser Ala Ile Asp Leu Ala Pro Thr Pro
      423 305          310          315          320
E--> 425 cag tta aaa gaa aga tta gca tat gaa ttt aaa ggc cac tcg ttg ctg
      426 1008
      427 Gln Leu Lys Glu Arg Leu Ala Tyr Glu Phe Lys Gly His Ser Leu Leu
      428          325          330          335
E--> 430 caa gct gca cga gaa gct gat gtt act cga atc aaa aaa cat ctc tct
      431 1056
      432 Gln Ala Ala Arg Glu Ala Asp Val Thr Arg Ile Lys Lys His Leu Ser
      433          340          345          350
E--> 435 ctg gaa atg gtg aat ttc aag cat cct caa aca cat gaa aca gca ntg
      436 1104
W--> 437 Leu Glu Met Val Asn Phe Lys His Pro Gln Thr His Glu Thr Ala Xaa
      438          355          360          365
E--> 440 cat tgt gct gct gca tct cca tat ccc aaa aga aag caa ata tgt gaa
      441 1152
      442 His Cys Ala Ala Ala Ser Pro Tyr Pro Lys Arg Lys Gln Ile Cys Glu
      443      370          375          380
E--> 445 ctg ttg cta aga aaa gga gca amc atc aat gaa aag act aaa gaa ttc
      446 1200
W--> 447 Leu Leu Leu Arg Lys Gly Ala Xaa Ile Asn Glu Lys Thr Lys Glu Phe
      448 385          390          395          400
E--> 450 ttg act cct ctg cac gtg gca tct gag aaa gct cat aat gat rtt gtt
      451 1248
W--> 452 Leu Thr Pro Leu His Val Ala Ser Glu Lys Ala His Asn Asp Xaa Val
      453          405          410          415
E--> 455 gaa gta gtg gtg aaa cat gaa gca aag gtt aat gct ctg gat aat ctt
      456 1296
      457 Glu Val Val Val Lys His Glu Ala Lys Val Asn Ala Leu Asp Asn Leu
      458          420          425          430
E--> 460 ggt cag act tct cta cac aga gct gca tat tgt ggt cat cta caa acc
      461 1344
      462 Gly Gln Thr Ser Leu His Arg Ala Ala Tyr Cys Gly His Leu Gln Thr
      463      435          440          445
E--> 465 tgc cgc cta ctc ctg agc tat ggg tgt gat cct aac att ata tcc ctt
      466 1392
      467 Cys Arg Leu Leu Leu Ser Tyr Gly Cys Asp Pro Asn Ile Ile Ser Leu
      468      450          455          460
E--> 470 cag ggc ttt act gct tta cag atg gga aat gaa aat gta cag caa ctc

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471 1440
472 Gln Gly Phe Thr Ala Leu Gln Met Gly Asn Glu Asn Val Gln Gln Leu
473 465                470                475                480
E--> 475 ctc caa gag ggt atc tca tta ggt aat tca gag gca gac aga caa ttg
476 1488
477 Leu Gln Glu Gly Ile Ser Leu Gly Asn Ser Glu Ala Asp Arg Gln Leu
478                485                490                495
E--> 480 ctg gaa gct gca aag gct gga gat gtc gaa act gta aaa aaa ctg tgt
481 1536
482 Leu Glu Ala Ala Lys Ala Gly Asp Val Glu Thr Val Lys Lys Leu Cys
483                500                505                510
E--> 485 act gtt cag agt gtc aac tgc aga gac att gaa ggg cgt cag tct aca
486 1584
487 Thr Val Gln Ser Val Asn Cys Arg Asp Ile Glu Gly Arg Gln Ser Thr
488                515                520                525
E--> 490 cca ctt cat ttt gca gct ggg tat aac aga gtg tcc gtg gtg gaa tat
491 1632
492 Pro Leu His Phe Ala Ala Gly Tyr Asn Arg Val Ser Val Val Glu Tyr
493                530                535                540
E--> 495 ctg cta cag cat gga gct gat gtg cat gct aaa gat aaa grr gsc ctt
496 1680
W--> 497 Leu Leu Gln His Gly Ala Asp Val His Ala Lys Asp Lys Xaa Xaa Leu
498 545                550                555                560
E--> 500 gta cct ttg cac aat gca tgt tct tat gga cat tat gaa gtt gca gaa
501 1728
502 Val Pro Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu Val Ala Glu
503                565                570                575
E--> 505 ctt ctt gtt aaa cat gga gca gta gtt aat gta gct gat tta tgg aaa
506 1776
507 Leu Leu Val Lys His Gly Ala Val Val Asn Val Ala Asp Leu Trp Lys
508                580                585                590
E--> 510 ttt aca cct tta cat gaa gca gca gca aaa gga aaa tat gaa att tgc
511 1824
512 Phe Thr Pro Leu His Glu Ala Ala Ala Lys Gly Lys Tyr Glu Ile Cys
513                595                600                605
E--> 515 aaa ctt ctg ctc cag cat ggt gca gac cct aca aaa aaa aac agg gat
516 1872
517 Lys Leu Leu Leu Gln His Gly Ala Asp Pro Thr Lys Lys Asn Arg Asp
518                610                615                620
E--> 520 gga aat act cct ttg gat ctt gtt aaa gat gga gat aca gat att caa
521 1920
522 Gly Asn Thr Pro Leu Asp Leu Val Lys Asp Gly Asp Thr Asp Ile Gln
523 625                630                635                640
E--> 525 gat ctg ctt agg gga gat gca gct ttg cta gat gct gcc aag aag agt
526 1968
527 Asp Leu Leu Arg Gly Asp Ala Ala Leu Leu Asp Ala Ala Lys Lys Ser
528                645                650                655
E--> 530 tgt tta gcc aga gtg aag aag ttg tct tct cct gat aat gta aat tgc
531 2016

```


RAW SEQUENCE LISTING

DATE: 10/24/2002

PATENT APPLICATION: US/10/019,980A

TIME: 16:07:59

Input Set : A:\EP.txt

Output Set: N:\CRF4\10242002\J019980A.raw

```

532 Cys Leu Ala Arg Val Lys Lys Leu Ser Ser Pro Asp Asn Val Asn Cys
533          660          665          670
E--> 535 cgc gat acc caa ggc aga cat tca aca cct tta cat tta gca gct ggt
536 2064
537 Arg Asp Thr Gln Gly Arg His Ser Thr Pro Leu His Leu Ala Ala Gly
538          675          680          685
E--> 540 tat aat aat tta gaa gtt gca gag tat ttg tta caa cac gga gct gat
541 2112
542 Tyr Asn Asn Leu Glu Val Ala Glu Tyr Leu Leu Gln His Gly Ala Asp
543          690          695          700
E--> 545 gtg aat gcc caa gac aaa gga gga ctt att cct tta cat aat gca gca
546 2160
547 Val Asn Ala Gln Asp Lys Gly Gly Leu Ile Pro Leu His Asn Ala Ala
548 705          710          715          720
E--> 550 tct tac ggg cat gta gat gta gca gct cta cta ata aag tat aat gca
551 2208
552 Ser Tyr Gly His Val Asp Val Ala Ala Leu Leu Ile Lys Tyr Asn Ala
553          725          730          735
E--> 555 tgt gtc aat gcc acg gac aaa tgg gct ttc aca cct ttg cac gaa gca
556 2256
557 Cys Val Asn Ala Thr Asp Lys Trp Ala Phe Thr Pro Leu His Glu Ala
558          740          745          750
E--> 560 gcc caa aag gga cga aca cag ctt tgt gct ttg ktg cta gcc cat gga
561 2304
W--> 562 Ala Gln Lys Gly Arg Thr Gln Leu Cys Ala Leu Xaa Leu Ala His Gly
563          755          760          765
E--> 565 gct gac ccg act ctt aaa aat cag gaa gga caa aca cct tta gat tta
566 2352
567 Ala Asp Pro Thr Leu Lys Asn Gln Glu Gly Gln Thr Pro Leu Asp Leu
568 770          775          780
E--> 570 gtt tca gcg gat gat gtc agc gct ctt ctg aca gca gcc atg ccc cca
571 2400
572 Val Ser Ala Asp Asp Val Ser Ala Leu Leu Thr Ala Ala Met Pro Pro
573 785          790          795          800
E--> 575 tct gct ctg ccc tct tgt tac aag cct caa gtg ctc aat ggt gtg aga
576 2448
577 Ser Ala Leu Pro Ser Cys Tyr Lys Pro Gln Val Leu Asn Gly Val Arg
578          805          810          815
E--> 580 agc cca gga gcc act gca gat gct ctc tct tca ggt cca tct agc cca
581 2496
582 Ser Pro Gly Ala Thr Ala Asp Ala Leu Ser Ser Gly Pro Ser Ser Pro
583          820          825          830
E--> 585 tca agc ctt tct gca gcc agc agt ctt gac aac tta tct ggg agt ttt
586 2544
587 Ser Ser Leu Ser Ala Ala Ser Ser Leu Asp Asn Leu Ser Gly Ser Phe
588          835          840          845
E--> 590 tca gaa ctg tct tca gta gtt agt tca agt gga aca gag ggt gct tcc
591 2592
592 Ser Glu Leu Ser Ser Val Val Ser Ser Ser Gly Thr Glu Gly Ala Ser

```


RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/019,980A

DATE: 10/24/2002

TIME: 16:07:59

Input Set : A:\EP.txt

Output Set: N:\CRF4\10242002\J019980A.raw

```

      593      850      855      860
E--> 595 agt ttg gag aaa aag gag gtt cca gga gta gat ttt agc ata act caa
596 2640
597 Ser Leu Glu Lys Lys Glu Val Pro Gly Val Asp Phe Ser Ile Thr Gln
598 865      870      875      880
E--> 600 ttc gta agg nat ctt gga ctt gag cac cta atg gat ata ttt gag aga
601 2688
W--> 602 Phe Val Arg Xaa Leu Gly Leu Glu His Leu Met Asp Ile Phe Glu Arg
603      885      890      895
E--> 605 gaa cag atc act ttg gat gta tta gtt gag atg ggg cac aag gag ctg
606 2736
607 Glu Gln Ile Thr Leu Asp Val Leu Val Glu Met Gly His Lys Glu Leu
608      900      905      910
E--> 610 aag gag att gga atc aat gct tat gga cat agg cac aaa cta att aaa
611 2784
612 Lys Glu Ile Gly Ile Asn Ala Tyr Gly His Arg His Lys Leu Ile Lys
613      915      920      925
E--> 615 gga gtc gag aga ctt atc tcc gga caa caa ggt ctt aac cca tat tta
616 2832
617 Gly Val Glu Arg Leu Ile Ser Gly Gln Gln Gly Leu Asn Pro Tyr Leu
618      930      935      940
E--> 620 act ttg aac acc tct ggt agt gga aca att ctt ata gat ctg tct cct
621 2880
622 Thr Leu Asn Thr Ser Gly Ser Gly Thr Ile Leu Ile Asp Leu Ser Pro
623 945      950      955      960
E--> 625 gat gat aaa gag ttt cag tct gtg gag gaa gag atg caa agt aca gtt
626 2928
627 Asp Asp Lys Glu Phe Gln Ser Val Glu Glu Glu Met Gln Ser Thr Val
628      965      970      975
E--> 630 cga gag cac aga gat gga ggt cat gca ggt gga atc ttc aac aga tac
631 2976
632 Arg Glu His Arg Asp Gly Gly His Ala Gly Gly Ile Phe Asn Arg Tyr
633      980      985      990
E--> 635 aat att ctc aag att cag aag gtt tgt aac aag aaa cta tgg gaa aga
636 3024
637 Asn Ile Leu Lys Ile Gln Lys Val Cys Asn Lys Lys Leu Trp Glu Arg
638      995      1000      1005
E--> 640 tac act cac cgg aga aaa gaa gtt tct gaa gaa aac cac aac cat
641 3069
642 Tyr Thr His Arg Arg Lys Glu Val Ser Glu Glu Asn His Asn His
643      1010      1015      1020
E--> 645 gcc aat gaa cga atg cta ttt cat ggg tct cct ttt gtg aat gca
646 3114
647 Ala Asn Glu Arg Met Leu Phe His Gly Ser Pro Phe Val Asn Ala
648      1025      1030      1035
E--> 650 att atc cac aaa ggc ttt gat gaa agg cat gcg tac ata ggt ggt
651 3159
652 Ile Ile His Lys Gly Phe Asp Glu Arg His Ala Tyr Ile Gly Gly
653      1040      1045      1050

```


RAW SEQUENCE LISTING

DATE: 10/24/2002

PATENT APPLICATION: US/10/019,980A

TIME: 16:07:59

Input Set : A:\EP.txt

Output Set: N:\CRF4\10242002\J019980A.raw

```

E--> 655 atg ttt gga gct ggc att tat ttt gct gaa aac tct tcc aaa agc
      656 3204
      657 Met Phe Gly Ala Gly Ile Tyr Phe Ala Glu Asn Ser Ser Lys Ser
      658 1055 1060 1065
E--> 660 aat caa tat gta tat gga att gga gga ggt act ggg tgt cca gtt
      661 3249
      662 Asn Gln Tyr Val Tyr Gly Ile Gly Gly Gly Thr Gly Cys Pro Val
      663 1070 1075 1080
E--> 665 cac aaa gac aga tct tgt tac att tgc cac agg cag ctg ctc ttt
      666 3294
      667 His Lys Asp Arg Ser Cys Tyr Ile Cys His Arg Gln Leu Leu Phe
      668 1085 1090 1095
E--> 670 tgc cgg gta acc ttg gga aag tct ttc ctg cag ttc agt gca atg
      671 3339
      672 Cys Arg Val Thr Leu Gly Lys Ser Phe Leu Gln Phe Ser Ala Met
      673 1100 1105 1110
E--> 675 aaa atg gca cat tct cct cca ggt cat cac tca gtc act ggt agg
      676 3384
      677 Lys Met Ala His Ser Pro Pro Gly His His Ser Val Thr Gly Arg
      678 1115 1120 1125
E--> 680 ccc agt gta aat ggc cta gca tta gct gaa tat gtt att tac aga
      681 3429
      682 Pro Ser Val Asn Gly Leu Ala Leu Ala Glu Tyr Val Ile Tyr Arg
      683 1130 1135 1140
E--> 685 gga gaa cag gct tat cct gag tat tta att act tac cag att atg
      686 3474
      687 Gly Glu Gln Ala Tyr Pro Glu Tyr Leu Ile Thr Tyr Gln Ile Met
      688 1145 1150 1155
E--> 690 agg cct gaa ggt atg gtc gat gga
      691 3498
      692 Arg Pro Glu Gly Met Val Asp Gly
      693 1160 1165
1047 <210> SEQ ID NO: 6
1048 <211> LENGTH: 19
1049 <212> TYPE: DNA
1050 <213> ORGANISM: Artificial Sequence
1052 <220> FEATURE:
1053 <223> OTHER INFORMATION: PCR Primers
1055 <400> SEQUENCE: 6
E--> 1056 cccgagagct gttcgaggc
      1057 19
      1060 <210> SEQ ID NO: 7
      1061 <211> LENGTH: 23
      1062 <212> TYPE: DNA
      1063 <213> ORGANISM: Artificial Sequence
      1065 <220> FEATURE:
      1066 <223> OTHER INFORMATION: PCR Primers
      1068 <400> SEQUENCE: 7
E--> 1069 caatctttac tctgttatat cct

```


RAW SEQUENCE LISTING

DATE: 10/24/2002

PATENT APPLICATION: US/10/019,980A

TIME: 16:07:59

Input Set : A:\EP.txt

Output Set: N:\CRF4\10242002\J019980A.raw

```
1070 23
1073 <210> SEQ ID NO: 8
1074 <211> LENGTH: 41
1075 <212> TYPE: DNA
1076 <213> ORGANISM: Artificial Sequence
1078 <220> FEATURE:
1079 <223> OTHER INFORMATION: PCR Primers
1081 <400> SEQUENCE: 8
E--> 1082 aagcggccgc attatggaaa ggatcatgtc gggtcgccgc t
1083 41
1086 <210> SEQ ID NO: 9
1087 <211> LENGTH: 25
1088 <212> TYPE: DNA
1089 <213> ORGANISM: Artificial Sequence
1091 <220> FEATURE:
1092 <223> OTHER INFORMATION: PCR Primers
1094 <400> SEQUENCE: 9
E--> 1095 aaggatccac cataccttca ggcct
1096 25
1099 <210> SEQ ID NO: 10
1100 <211> LENGTH: 39
1101 <212> TYPE: DNA
1102 <213> ORGANISM: Artificial Sequence
1104 <220> FEATURE:
1105 <223> OTHER INFORMATION: PCR Primers
1107 <400> SEQUENCE: 10
E--> 1108 aaaagcttta tggaaaggat catgtcgggt cgccgctgc
1109 39
```


VERIFICATION SUMMARY

DATE: 10/24/2002

PATENT APPLICATION: US/10/019,980A

TIME: 16:08:00

Input Set : A:\EP.txt

Output Set: N:\CRF4\10242002\J019980A.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:34 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:1
L:47 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:2
L:69 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:3
M:254 Repeated in SeqNo=3
L:123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:1080
L:201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2640
L:318 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:309
L:325 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:4
M:254 Repeated in SeqNo=4
L:435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:1056
L:437 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:1104
L:447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:1200
L:452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:1248
L:497 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:1680
L:562 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:2304
L:600 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:2640
L:602 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:2688
L:839 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:352
L:847 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:384
L:851 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:400
L:887 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:544
L:939 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:752
L:971 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:880
L:1056 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:6
L:1069 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:7
L:1082 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:41 SEQ:8
L:1095 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:9
L:1108 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:39 SEQ:10